REMARKS

I. *Status of the Claims*

Claims 3, 5, 13, and 44-57 are pending. Claims 1-2, 4, 6-12, and 14-43 were previously canceled without prejudice or disclaimer. Applicants reserve the right to file one or more continuing applications to the canceled subject matter. Claims 56 and 57 are withdrawn for allegedly falling outside the scope of the elected restriction Group. Claims 3, 13, 44, 49, 50-52 and 54 are amended for the reasons related in the following section.

(a) Interview with Examiner Fox, January 3, 2007

Applicants thank Examiner Fox for extending the courtesy of a personal interview with Applicants' representatives on January 3, 2007, to discuss the merits of this case and for his constructive feedback. See the Interview Summary of January 9th, which memorializes Examiner Fox's suggestion to amend claim 3 to clarify what is a border-like sequence. Pursuant to that advice, Applicants hereby amend claim 3 to make more explicit that the previously-recited "border-like" sequence is a sequence "from a plant that promotes and facilitates integration of the desired polynucleotide into the plant genome and which is not a T-DNA border." Support for this amendment is found, for instance, in paragraph 44, which spans pages 18-19, and paragraph 213 which bridges pages 57 and 58. It is evident throughout the specification that the border-*like* sequence is not identical in nucleotide sequence to any Agrobacterium T-DNA border sequence. See the opening line of paragraph 45 at page 19.

Examiner Fox also suggested that Applicants amend claim 13 to reflect that the claimed progeny plant comprises a border-like sequence from a plant which is operably linked to or flanking a nucleic acid. See the Interview Summary. To expedite a favorable consideration, Applicants hereby amend claim 13 as suggested by Examiner Fox. Thus, claim 13 requires the progeny plant to have in its genome a desired polynucleotide that is operably linked to 5-100 nucleotides of a plant sequence that promotes and facilitates integration of a polynucleotide to which it is linked into a plant genome, wherein the plant sequence is not a T-DNA border. Support for the 5-100 nucleotide range for the size of the plant sequence

that is operably linked to the desired polynucleotide is found explicitly at the top of page 19. That the desired polynucleotide is operably linked to the border-like element is found throughout the specification, but please see exemplary support at paragraph 48 at page 20 and paragraph 159 at page 44. By way of this amendment, claim 13 no longer is written in the objectionable product-by-process language. Furthermore, claim 13 comports with claim 3 in that it clarifies what is a border-like sequence in keeping with Examiner Fox's suggestion.

(b) Claim amendment support

Claim 3	- paragraph 44 (pages 18-19) - paragraph 213 (pages 57-58) - paragraph 45 (page 19)
Claim 13	- paragraph 44 (pages 18-19) - paragraph 48 (page 20) - paragraph 159 (page 44)
Claims 44, 49, 50-52, 54	- deletes "selectable" and thereby ensures correct antecedent basis with claim 3's "marker gene."

None of these amendments introduces new subject matter and therefore Applicants respectfully request their entry.

II. *The recitation of "marker gene" in claims 3, 13, and 53 does not introduce new matter because the specification provides basis and literal support for that component*

Claims 3, 13, and 53 are rejected under 35 U.S.C. § 112, first paragraph as allegedly introducing new matter because the Office cannot identify support in the specification for "marker gene" as opposed to the originally-recited "*selectable* marker gene" (emphasis added).

Applicants respectfully point out that the term "marker gene" is literally present throughout the original specification and therefore the "new matter" rejection is moot. Applicants direct the Office to paragraph 18 at page 9 ("Conventional ***marker genes*** are incorporated into genetic constructs and used to select for transformation events"); paragraph 20 at page 9 (". . .the ***marker gene***

and desired gene or nucleotide sequence are placed on different vectors"); paragraph 28 at page 12 ("a transgenic plant . . . does not comprise a non-plant species ***marker gene***"); paragraph 32 at page 13 ("Other ***marker genes*** include" and "It is well known in the art how to follow expression of such ***marker genes*** to determine whether or not the ***marker gene*** has been stably expressed into the genome of a transformed plant cell"); paragraph 36 at page 15 ("and a LifeSupport vector, which contains ***a marker gene***. The ***marker gene*** may, or may not, be inserted between P-DNA border-like sequences, T-DNA border sequences, or other T-DNA-like border sequences"); paragraph 38 at page 15 ("the plant-derived ***marker gene***"); paragraph 63 at page 22 ("a LifeSupport vector that comprises a ***marker gene*** flanked by a T-DNA left border and a T-DNA right border"); paragraph 126 at page 34 ("backbone integration ***marker gene***"); and so on.

Applicants also have amended claims 44, 49, 50-52 and 54 to delete "selectable" and thereby ensure those claims are correctly antecedent with respect to claim 3's "marker gene" component.

Accordingly, Applicants assert the specification provides basis for the term "marker gene" and therefore recitation of that term in the claims does not introduce new matter. Applicants therefore respectfully ask the Office to withdraw the rejection.

III. *Lilly does not require, legally or logically, that Applicants define a generic nucleotide element by a precise nucleotide sequence or with a corresponding consensus sequence and, therefore, claims 3, 5, 13, and 44-55 do not lack written description for reciting "border-like"*

The Office maintains the rejection of claims 3, 5, 13, and 44-55 under 35 U.S.C. § 112, first paragraph as broadly drawn to a genus of border-like sequences of any sequence from any plant. Office action at pages 3-4. The Office's position is that "[N]o particular consensus sequence of any length is recited in the claims. Thus, the claims do not recite a genus of sequences which is commensurate in scope with what was exemplified." Action at page 4. The Office further posits that "the claims do not recite the structure (consensus sequence) allegedly correlated with function (ability to transfer foreign DNA into the recipient plant genome) as

required by [*Regents of the University of California vs. Eli Lilly and Company*, 119 F.3d 1559 (1997)]." Action at page 4.

Applicants respectfully assert that the Office's reliance on *Lilly* is moot because the claims no longer recite the "border-like" element for the reasons related in § I (a) above and primarily in response to Examiner Fox's suggestion to explicitly explain that claimed element. Applicants take this opportunity, however, to address the Office's rationale for employing the *Lilly* case law.

(i) *Under Lilly, the precise definition of a claimed DNA may be made by reciting its "structure, formula, chemical name, or physical properties"*

The issue in *Lilly* concerned whether or not a claim drawn to a *human* proinsulin gene met the written description when the specification only described the *rat* proinsulin sequence.

Applicants respectfully disagree that *Lilly* requires reciting a precise nucleotide sequence when there is a representative number of nucleotide species to evince existence of the corresponding genus. Applicants contend that, unlike the specific human proinsulin gene in contention in *Lilly*, the plain words "border-like" readily conveys distinguishing information concerning the identity of the underlying DNA sequences. The person of ordinary skill in the art would have been readily able to visualize and recognize the identity of the various sequence members of the "border-like" genus simply because, as the skilled artisan, he would have appreciated what was a "border-like sequence." It is a sequence that has a sequence "like" a T-DNA border sequence.

Lilly reiterated that a claimed DNA "requires a precise definition ***such as*** by structure, formula, ***chemical name***, ***or physical properties***" (emphasis added, *Id.* at 1566). Thus, contrary to the Office's more-limited reading, *Lilly* does not circumscribe only one means for advancing a claim drawn to a DNA molecule. Rather, *Lilly* says that the "precise definition" may be satisfied by enunciating any one of the DNA molecule's (1) structure, (2) formula, (3) chemical name, or (4) its physical properties. Applicants are therefore not limited to only the "structural" option in order to define their claimed DNA sequence.

Indeed, the Court in *Amgen v. Hoechst Marion Roussel*, 314 F.3d 1313 (2003), reiterated that the *Lilly* decision did not outright eliminate the possibility that *functional* descriptions of genetic material could be used to satisfy the written description requirement. "The requirement may be satisfied if in the knowledge of the art the disclosed function is sufficiently correlated to a particular, known structure." *Amgen* at 1332. The supposed ambiguity in *Amgen* lay in identifying types of cells, not, as in *Lilly*, identifying an unknown and unspecified nucleotide sequence. The Court held that "the words 'vertebrate' [cells] and 'mammalian' [cells] readily convey distinguishing information concerning [their] identity such that one of ordinary skill in the art could visualize or recognize the identity of the members of the genus." *Id.* Hence, in *Amgen*, "vertebrate cells" and "mammalian cells" were words that sufficiently connoted the recited cellular genus. It was unnecessary to specify anything more about those particular cells because *the words alone* were unambiguous and would not have bewildered the skilled artisan.

By the same token, the Office cannot contend that, among those who work in the field of *Agrobacterium*-mediated transformation, the conventional ***name*** "T-DNA border" would have confused the skilled person as to the structure or function of that particular DNA molecule. To be sure, the person of ordinary skill in the art knows full well what is a T-DNA left border and what is a T-DNA right border, in much the same way as the skilled person knows what is meant by vertebrate and mammalian cells. The skilled person, in this case, would know what are the ***physical properties*** of those conventional T-DNA borders without having to know the precise nucleotide sequences of the left and right borders. That is, the skilled person knows that these conventional borders act as enzyme recognition sites in the context of *Agrobacterium*-mediated transformation.

Similarly, an applicant typically is not required to first recite the entire sequence of an *Agrobacterium* transformation *vector* before the associated method claim is found allowable; even though it probably is the case that different transformation methods employ different transformation vectors. Yet despite the use of different vectors, the Office accepts that it is unnecessary to recite the exact sequences of the vectors in question, because, like *Amgen's* cells, the word "vector"

alone identifies the genus of vectors that the skilled person can employ to perform *Agrobacterium*-mediated transformation.

The vectors are tools. Likewise, T-DNA borders and border-like elements are tools. In the context of conventional T-DNA borders, the Office does not require an applicant to recite the exact nucleotide sequence of that T-DNA border component, which is identified in a claim only by its conventional name.

Accordingly, based on the plain meaning of "border-like" in the context of *Agrobacterium*-mediated transformation, the skilled person would immediately understand that Applicants' claimed invention employs a sequence that is structurally and functionally "like," but not identical to, a conventional T-DNA border. The specification only verifies that immediate understanding. The specification is not limiting with respect to *which* particular border-like sequences are useful for performing the claimed method.

Indeed, the skilled artisan knows, or can easily find, the nucleotide sequences of known *Agrobacterium* T-DNA borders. The inventors determined that there are border-like sequences in the plant genome that, when isolated, can be used as T-DNA borders. These border-like sequences do not have nucleotide sequences that are identical to known *Agrobacterium* T-DNA borders.

In the same vein as the precedent and Office practice, therefore, Applicants should not have to recite a specific nucleotide sequence or the consensus sequence of the tool they call a "border-like" sequence. Applicants invoke the reasoning in *Amgen* that "border-like" readily conveys distinguishing information concerning the identity of the members of the border-like genus without having to necessarily recite any nucleotide structure. This is especially the case since claim 3 already does comply with the other non-structural *Lilly* "requirement" of defining the border-like element by its physical properties.

Moreover, unlike in *Lilly*, Applicants *have* provided sufficient representative species of border-like sequences. Applicants relate numerous border-like sequences, which not only create a consensus but which also justify the existence of the "border-like" genus without having to resort to any precise recitation of the

nucleotide sequence/consensus. By contrast, in *Lilly*, the human proinsulin sequence was missing entirely from the specification.

(ii) *Lilly breached the written description boundary by creating a "super-enablement" standard that specifically penalizes biotech applicants*

In his concurring opinion in *Moba* v. *Diamond Automation*, 325 F.3d 1306, Justice Rader said that *Lilly* is an "erroneous written description requirement [which] lacks both a statutory and logical foundation." *Id.* at 1323. *Moba* concerned software claims for controlling high-speed egg processors. The patent was found not invalid because the specification adequately described every component in "sufficient detail." Plus, requiring "some experimentation . . . to practice the claimed invention is permissible, so long as it is not undue." *Id.* at 1321.

With that background, J. Rader said that *Lilly* requires "more disclosure than necessary to enable one of skill in the art to make and use the invention," and that *Lilly* breached the written description line by creating a "super-enablement" standard. *Id.* at 1325. For biotechnology inventions, Rader said, this super-standard "presents severe consequences." *Id.* "*Lilly* purports to require the recitation, nucleotide by nucleotide, of the entire sequence . . . [T]his non-statutory rule jeopardizes the validity of many inventions in biotechnology." *Id.* Furthermore, *Lilly* "may tax a [patent] drafter beyond reasonable limits. A new protein or other DNA-related discovery may contain hundreds of [residues]. Consequently, a 'precise definition' . . . as required by *Lilly*, apparently requires tedious disclosure of thousands of potential permutations . . . that all fall within a proper description of the . . . DNA source." *Id.* The *Lilly* rule improperly imposes technology-specific written description requirements.

> In sum, the *Lilly* rule is not just a mere one-time mistake. It defies over thirty years of case law. It finds no specific support in any statutory language. It creates a technology-specific rule in a technology-neutral statute. It distorts the statute's rules for adequate disclosure of inventions. It complicates biotechnology patent drafting to the point of near impossibility and invites invalidating mistakes. It prices non-corporate inventors out of some biotechnological invention markets. Last, but not least, it burdens both trial and appellate courts with unnecessary and confusing procedures in otherwise simple cases like this one. (*Id.* at 1326-1327).

(iii) *The question is not whether there is a qualified genus of border-like sequences described by the specification but whether recitation of "border-like" is an appropriate way to express that genus in the claims*

The present invention is a simple and elegant case. Applicants have invented a novel method for transforming plants that the Office acknowledges is unprecedented in the prior art. Action at page 7. Yet, the application is mired in non-existent ambiguities concerning the meaning of "border-like sequence."

There are two things going on. The first concerns whether the specification provides a sufficient number of representative "border-like" sequence members to justify the existence of the corresponding genus. No doubt, the specification does so provide a representative number of border-like sequences. See for instance Table 2 at pages 54-55. Thus, in this regard, the claimed invention is consistent with *Lilly*, in which the Court said that the applicant "must describe a representative number of the species of the claimed genus." See page 9 of the non-final Office Action dated May 23, 2006.

The second thing, however, concerns an undue focus on *how Applicants should recite that genus in the claims*. The Office says that Applicants need to recite the consensus sequences, *e.g.*, SEQ ID NOs. 47 or 93, in order to adequately describe the genus. Applicants say that, actually, the description of the genus is satisfied by the recitation of the generic name, "border-like sequence." Applicants assert that it is unnecessary and improper to recite the consensus sequences *verbatim* in order to adequately describe the border-like genus. As made clear in the preceding passages, the term "border-like" is impregnated with a meaning that is readily understood by all of those who practice *Agrobacterium*-mediated plant transformation. Applicants reiterate that Lilly is moot because "border-like" no longer is recited in any of the claims.

If the Office's position and construction of *Lilly* was the truly correct pronouncement of the written description requirement, then no claim that recited a conventional "T-DNA border" could ever issue unless the claim also recited a corresponding sequence or consensus. Plus, one could not claim a genus of T-DNA borders unless the specification disclosed a representative number of T-DNA sequences. If that disclosure was lacking, however, then by the Office's rationale

the T-DNA border would have to be limited to the specific sequence(s) disclosed in the specification. But if those sequences were omitted from the specification, then from the Office's perspective that claim would be fatally defective because it could never satisfy Lilly's "precise definition" as construed by the Office. Clearly, such a strict and narrow description of a nucleotide genus has never been a threshold requirement under U.S. patent law.

Indeed, patents *have* issued which recite nothing more than "T-DNA border sequence" language unaccompanied by any specific sequence or functional language. See, for instance, [the arbitrarily-picked] claim 1 of United States Patent No. 7,112,721 ("*introducing into plant cells a construct comprising, in the 5' to 3' direction: a right Agrobacterium* ***T-DNA border sequence*** "); claim 7 of USP 7,060,876 ("*the Agrobacterium bacterium comprises a vector comprising at least one virulence gene of a Ti plasmid, a* ***left T-DNA border***, *a* ***right T-DNA border***"); and claim 1 of USP 7,026,529 ("*an antibiotic selection marker operably linked to at least* ***one T-DNA border*** ").

Furthermore, the Office recognizes that there exist underlying consensus sequence issues for *other* nucleotide elements. See Table 5 under Section 2422 of the MANUAL OF PATENT EXAMINING PROCEDURE. There, for example, the Office asserts that a "polyA_signal" is a recognition region that has a "consensus=AATAAA"; likewise it says that a "GC_signal" is a GC-rich region that has a "consensus=GGGCGG"; and that the "CAAT_signal" is commonly known as the CAAT box, which has a "consensus=GG(C or T)CAATCT"; and that the "TATA box" has a "consensus=TATA(A or T)A(A or T)."

Yet, U.S. patents have issued with claims that recite those generic terms but which do not recite the corresponding consensus sequence. See claim 9 of USP 6,878,530 ("*wherein said first and said second partial duplexes comprise* ***GC-rich sequences***"); claim 6 of USP 7,135,562 ("*[T]he isolated nucleic acid of claim 1 further comprising a* ***polyadenylation signal sequence***"); and claim 4 of USP 7,078,234 ("*[A] transgenic plant according to claim 1 wherein said promoter comprises* ***CAAT and TATA box elements***") (emphases added). By the Office's rationale none of claims 9, 6, and 4 of these patents, nor the "T-DNA border" patents, satisfy *Lilly*

because none of the claims recite the corresponding consensus sequence; they only generically recite "T-DNA borders," "GC-rich" sequences, "polyadenylation signal" sequences and "CAAT and TATA box" sequences.

Accordingly, the Office's rationale that permits the recitation of those generic elements is the same rationale that underlies Applicants contention that "border-like" is sufficient to meet the written description requirement without necessarily having to recite any of the disclosed consensuses. To be clear, *Lilly* does not mandate, legally or logically, any requirement that a recited named sequence must be accompanied by a precise nucleotide sequence or a corresponding border-like consensus. For these reasons, as well as those outlined above, Applicants respectfully request withdrawal of this rejection.

(iv) *A genus may encompass non-functional species*

The Office further contends that Applicants' own work, as evidenced by Rommens *et al.*, *Plant Physiology*, Vol. 139, pp. 1338-1349, November, 2005, shows that "of the 41 putative 'border-like' sequences . . . almost one-half failed to effect foreign DNA integration into tobacco genomes transformed therewith." Action at page 4. Applicants also point to their discussion of *Atlas Powder* in § IV below that a claimed genus may encompass inoperative embodiments.

Applicants assert at the outset that the claimed invention does not call for the use of each and every border-like genus member; it only calls for the use of those border-like sequence members that are (a) not T-DNA borders and (b) functionally promote and facilitate polynucleotide integration. The latter defines the "physical property" requirement *a la Lilly* and is sufficient to meet the written description requirement. Secondly, this classifies the useful genus as containing those border-like members which are functional. A sequence that looks like a border-like element, but which is not functional, does not meet the claim.

Applicants teach how to determine whether or not a border-like sequence is functional. The specification accurately and clearly teaches methods for (1) identifying and isolating a border-like sequence; such as by (i) searching DNA databases and (ii) employing the polymerase chain reaction (PCR) to identify

sequences that satisfy the inventive "border-like" criteria; and (2) testing the functionality of a border-like sequence by infecting an explant with an *Agrobacterium* transformation plasmid that lacks conventional T-DNA borders but which contains one or two border-like sequences and a gene marker expression cassette. If the border-like sequence(s) is functional, in a transformation sense, then the gene marker, such as the neomycin phosphotransferase (*nptII*) gene, will be integrated into the explant genome. In the case of nptII, it will be readily apparent that integration has occurred by the subsequent formation of kanamycin resistant calli.

The present situation is not a case whereby only one border-like sequence is described in the specification and no other species, like the case in *Lilly* (only rat proinsulin sequence described). Applicants actually provided here a representative number of subgenus members that work. More importantly, however, with respect to genus/species relationships, the written description requirement does not require that every species of a genus functions. The genus does not fall apart simply because there exist non-functional member species. Accordingly, Applicants respectfully request withdrawal of the rejection for this reason too.

(v) *Bayer is of no avail because the skilled person necessarily must conduct some assay testing to identify and use non-disclosed species that nonetheless fall within the claimed genus in order to practice the claimed invention*

The Office also cited *Bayer* v. *Housey*, 340 F.3d 1367 for the proposition that an assay for finding a product is not equivalent to a positive recitation of how to make a product. Action at page 4. That proposition, however, commingles three things, namely, (1) how to identify species of border-like sequences that comport with the functional and consensus descriptions disclosed in the specification, with (2) how to obtain those plant-specific border-like sequences, and with (3) how to test those border-like sequences for functional activity.

Since the written description requirement does not call for every single species of a genus to be recited in the specification in order to justify the genus, only a representative number, it necessarily is the case that the skilled person will

need to identify, obtain, and test *non-disclosed* species that nevertheless fall within the genus in question.

Applicants require nothing more of the skilled artisan than that. That is, this is not a case where the skilled person is at a loss as to how to perform the invention and therefore is forced to hunt down and arbitrarily pick and choose sequences that might fit into the border-like genus. To the contrary, the specification provides very clear guidelines and details concerning what the structure, *e.g.*, nucleotide sequence, of the border-like sequences should look like, as well as standard tests for testing the activity of that candidate sequence. If that was not enough, Applicants provide not one, but two consensus sequences, which delineate the structural position of certain nucleotides in that candidate sequence.

With all of this information, the skilled person would not be using the *Bayer*-style assay to *find*, out of the blue, a product that met the claimed requirements. Instead, the skilled person would be looking to the detailed guidance provided by the specification to identify alternative non-disclosed species that nevertheless fall within the border-like genus. That search would not impose any undue experimentation on the skilled person, because, as Applicants say, every skilled artisan interested in practicing a claimed invention necessarily has to look for non-disclosed species that fits the bill of the genus in question. The extent to which the skilled person needs to conjure up his own ideas and self-developed methods and tools for going about performing that method is what *Bayer* speaks about. The present specification in no way, however, leaves the skilled person floundering. Applicants' specification provides clear guideposts for identifying additional border-like sequences t for practicing their claimed method.

(vi) *Conclusion*

Thus, contrary to the Office's position, *Lilly* does not require or otherwise mandate recitation of a consensus sequence. That aside, Applicants no longer recite "border-like sequence" in the claims, which, in any event, is by itself sufficient to meet the written description guidelines. The Office does not require that each and every species of a genus work. Lastly *Bayer* is of no consequence here because it necessarily is the case that the skilled person would have to

conduct some assay tests, in accordance with the detailed description, to practice the claimed invention with non-disclosed species of border-like elements. For these reasons, Applicants respectfully request that the Office withdraw its rejection of the claims as lacking written description support.

IV. *Contrary to the Office's position, Atlas Powder does not outright prohibit "the majority of the claim from encompassing inoperative embodiments"*

As memorialized in the Interview Summary of January 9th, Examiner Fox indicated that the claimed invention also suffers from application of "Atlas Powder," which "prohibited the majority of the claim from encompassing inoperative embodiments, as apparently taught by Rommens *et al.*" Applicants assume the referenced case law is *Atlas Powder Co. v. E.I. Du Pont De Nemours & Co.*, 750 F.2d 1569 (1984). Applicants believe that the Office's characterization of *Atlas Powder* is over-reaching for the following reasons.

Atlas Powder concerned a patent drawn to blasting agents and chemical mixtures that can be detonated with high strength explosive primers. Du Pont began selling a blasting agent, whereupon Atlas sued for infringement. In its defense, Du Pont argued among other things that Atlas' claims were non-enabled. According to Du Pont, Atlas' disclosure was "nothing more than a 'list of candidate ingredients from which one skilled in the art would have to select and experiment unduly to find an operable emulsion." *Id.* at 1576.

The United States Court of Appeals, however, affirmed the District Court's conclusion that Atlas' claims *were* enabled because (a) "it would have been impossible for [the patentee] to list all operable emulsions and exclude the inoperable ones and (b) "such a list [is] unnecessary, because one skilled in the art would know how to select a salt and fuel and then apply [a basic principle of emulsion chemistry] to determine the proper emulsifier."

> ***Even if*** some of the claimed combinations were inoperative, ***the claims are not necessarily invalid***. "It is not a function of the claims to specifically exclude ... possible inoperative substances...." ... Of course, if the number of inoperative combinations ***becomes*** significant, and in effect forces one of ordinary skill in the art to experiment ***unduly*** in order to practice the claimed invention, the claims ***might*** indeed be invalid.

Id. at 1576-1577 (emphasis added).

Accordingly, *Atlas Powder* does not outright prohibit the majority of the claim from encompassing inoperative embodiments. Furthermore, Du Pont could not avail itself of Atlas' report that 40 percent of its experiments "failed," because those experimental "failures" simply reflected sub-optimal conditions. "Such optimality is not required for a valid patent." *Id.* at 1577. For the same reason, it is of no avail to the Office to say that Applicants' own post-filing date publication, Rommens (*supra*), reported that "sequence variation in said 'border-like' sequence reduced or inhibited activity in over half of the cases." Office action dated November 20, 2006, at page 6, and as reiterated in the Interview.

Moreover, in keeping with the Appellate Court's conclusions in *Atlas*, **(1)** it would be impossible for Applicants to list all operable border-like sequences and exclude all of the inoperable ones; **(2)** the skilled person knows, and is guided by Applicants' present specification, how to identify, isolate, and test candidate border-like sequences for appropriate functionality; and **(3)** the legal precedent does not automatically invalidate a claim that encompasses inoperative embodiments. Accordingly, it is too much to say that *Atlas Powder* prohibits inoperative embodiments. *Atlas Powder* does not undermine Applicants claimed invention.

V. *McElroy's "one nucleotide" is necessarily also a portion of a T-DNA border sequence, which violates the requirement of claim 13 that the portion of the border-like sequence, which is integrated into the plant genome is not a portion of a T-DNA border*

Claim 13 is rejected under 35 U.S.C. 102(e) as allegedly anticipated by United States Patent No. 6,750,379 ("McElroy"). Action at page 7. The reason is that "the claims read on any plant transformed with any plant-derived sequence, wherein said plants may comprise 1 base pair of a 5-25 base pair sequence of unspecified sequence." *Id.* Hence McElroy, which teaches maize plants containing a maize heat shock protein, "would inherently contain at least one additional base pair, which base pair would be indistinguishable from the defined 'portion' of a 'border-like' sequence." *Id.*

Applicants understand the rationale underlying this rejection, but respectfully disagree with the outcome. McElroy does *not* anticipate claim 13 because claim 13 also requires that the "portion" which resides in the transformed plant genome "does not have a nucleotide sequence identical to a portion of a T-DNA." McElroy's "one nucleotide" – be it an A, G, C, or T - *necessarily* is identical to "a portion of a T-DNA." Furthermore, claim 13 requires that the claimed progeny plant comprises a desired polynucleotide in its genome that is operably linked to 5-100 nucleotides of a plant sequence that promotes and facilitates integration of a polynucleotide to which it is linked into a plant genome. McElroy's one common nucleotide does not meet or anticipate that claimed requirement. Accordingly, McElroy does not anticipate claim 13. For this reason, Applicants respectfully request withdrawal of this rejection.

CONCLUSION

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested. The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

Respectfully submitted,

Date February 20, 2007

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